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ngspipelines.toulouse.inra.fr:9064/ngspipelines/report.jsp?id=2297&root=NGSpipelines&datasetType=srnaseq&plugin=locusreport&mart=Onchorhynchus\_mykiss-ncRNAMicrotrout

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# miRNA loci summary

MirNA\_219 General Information

- Name: miRNA\_219
- Type: miRNA
- Reference: scaffold\_1161
- Position: 139903 - 139962
- Strand: forward
- Length: 60
- Score: 1200

Export box

Export sequence | Export annotations

# miRNA structure

Sequence And Structure

Free energy: -14.3

Paired nucleotides: 38

Hairpin loop number: 1

Bulge number: 4

Single-base bulge number: 4

Unpaired nucleotides: 22

Hairpin loop max size: 15bp

Bulge max size: 1bp

Junction number: 0

Extract region from: 1 to 60 | Reset

Search nucleotide sequence:

miRNA\_219  
CATTATTAATT TTGGTACCGC GCTATGCCAA ACTCTACTCCG TACCGTGAGT AATATTCAC  
((((((((( ( (((((((( (.....))))))) ))))))))....

Seq. composition (GC%: 41.67)

A: 26.7% T: 31.7% C: 25.0% G: 16.7% Other: 0.0%

# miRNA annotation

Functional Annotation Best Hit

Accession: RF00701 (rfam-mirna)

Family: mir-126

Query start>end: 139903>139921

Evalue: 0.00006

% identity: 100

Species: none

Subject start>end: 47>65

Score: 38.2

Mismatches: 0

Structural Annotation

Type: Gene

Gene ID: GS0NMG0003428001

start>end: 123725>143837

Same strand?: yes

# miRNA isoforms

Features Table

Show 10 entries

Name	Score	Database	Start
RF00701	38.2	rfam-mirna	139903
MIMAT0036676	38.2	mirbase	139903

Showing 1 to 2 of 2 entries

First Previous 1 Next Last

Isoforms Table

Show 10 entries

Name	Nb_samples	Expression	Annotations	Sequence
seq1722	38	135373	mirbase:MIMAT00117.mir-126-5p;rfam-mirna:RF00701.mir-126	CATTATTAATT TTGGTACCGC
seq14504	38	290506	mirbase:MIMAT0035927.mir-126-5p;rfam-mirna:RF00701.mir-126	CATTATTAATT TTGGTACCGC
seq1723	38	284870	mirbase:MIMAT00117.mir-126-5p;rfam-mirna:RF00701.mir-126	CATTATTAATT TTGGTACCGC
seq16971	38	199901	mirbase:MIMAT0024207.mir-126-5p;rfam-mirna:RF00701.mir-126	CTGGTACCGCTGAGTAAATAGCC
seq23523	38	1173960	mirbase:MIMAT003588.mir-126-3p;rfam-mirna:RF00701.mir-126	TGGTACCGCTGAGTAAATAGCC
seq10113	38	64033	mirbase:MIMAT000445.mir-126-3p;rfam-mirna:RF00701.mir-126	TGGTACCGCTGAGTAAATAGCC
seq20445	38	1009794	mirbase:MIMAT0029400.mir-126a;rfam-mirna:RF00701.mir-126	TGGTACCGCTGAGTAAATAGCC
seq10451	38	59009	mirbase:MIMAT0029400.mir-126a;rfam-mirna:RF00701.mir-126	CCTGACCGTGAGTAAATAGCC
seq20100	37	2939	mirbase:MIMAT000137.mir-126a-5p;rfam-mirna:RF00701.mir-126	CAATTATCTTTGTGACCG
seq22605	37	21011	mirbase:MIMAT0035927.mir-126-5p;rfam-mirna:RF00701.mir-126	ATTATCACTTGTGACCG

Showing 1 to 10 of 24 entries

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Links

- GenoToul Bioinfo platform
- Sigenea platform
- INRA - National Institute for Agricultural Research

About NGS Pipelines

Second generation sequencing platforms provide new insight of the biological phenomena taking place in studied samples. NGS Pipelines is a set of workflows and a query and visualisation environment build upon biomart which aims at emptying biological knowledge extraction.

A FAQ is available to give some information about the most usual questions asked.

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